Amendments to The Claims

The following listing of claims replaces all prior versions and listings of the claims in this application.

Listing of the Claims

1-193. (Cancelled)

194. (Currently amended) A method for identifying a compound that potentially modulates a T1R2/T1R3 ~~(sweet)~~ receptor ~~associated taste in a subject~~ comprising:

(i) screening one or more compounds in a functional assay that detects compounds which modulate (enhance or inhibit) the activity of the T1R2/T1R3 receptor by another compound; and

(ii) identifying compounds that potentially modulate the T1R2/T1R3 receptor-~~associated taste~~ based on their modulation (enhancement or inhibition) of the activity of the T1R2/T1R3 ~~(sweet)~~ ~~taste~~ receptor by another compound, wherein said T1R2 is a T1R2 polypeptide and is (i) encoded by a nucleic acid sequence comprising SEQ. ID. NO: 10, (ii) encoded by a nucleic acid sequence comprising a nucleic acid that hybridizes to SEQ. ID. NO: 10 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS, or (iii) a T1R2 polypeptide possessing at least 90% sequence identity to the T1R2 polypeptide of SEQ. ID. NO: 6;

and wherein said T1R3 is a T1R3 polypeptide and is (i) encoded by a nucleic acid sequence comprising SEQ. ID. NO: 9 ~~or SEQ. ID. NO: 11~~; (ii) encoded by a nucleic acid sequence that hybridizes to SEQ. ID. NO: 9 ~~or SEQ. ID. NO: 11~~ under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, 10% SDS; and washing at 65°C in a solution comprising 0.2X SCC and 0.1% SDS, or (iii) a T1R3 polypeptide possessing at least 90% sequence identity to the T1R3 polypeptide of ~~SEQ. ID. NO: 4 or~~ SEQ. ID. NO: 7.

195. (Canceled)

196. (Previously presented) The method of claim 194 wherein said T1R2 and T1R3 are of the same species origin.

197. (Canceled)

198. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide comprising the amino acid sequence of SEQ. ID. NO: 6.

199. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide that exhibits at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 6.

200. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide that exhibits at least 95% sequence identity to the polypeptide of SEQ. ID NO: 6.

201. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide that exhibits at least 96% sequence identity to the polypeptide of SEQ. ID NO: 6.

202. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide that exhibits at least 97% sequence identity to the polypeptide of SEQ. ID NO: 6.

203. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide that exhibits at least 98% sequence identity to the polypeptide of SEQ. ID NO: 6.

204. (Previously presented) The method of claim 194 wherein said T1R2 is a human T1R2 polypeptide that exhibits at least 99% sequence identity to the polypeptide of SEQ. ID NO: 6.

205. (Previously presented) The method of claim 194 wherein said T1R2 is encoded by the nucleic acid sequence of SEQ. ID. NO: 10.

206. (Previously presented) The method of claim 194 which said T1R2 is encoded by a nucleic acid sequence that hybridizes to SEQ. ID. NO: 10 under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

207. (Canceled)

208. (Canceled)

209. (Previously presented) The method of claim 194 wherein said T1R3 is a human T1R3 polypeptide having the amino acid sequence of SEQ. ID. NO: 7.

210. (Previously presented) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 90% sequence identity to the polypeptide of SEQ. ID. NO: 7.

211. (Previously presented) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possess at least 95% sequence identity to the polypeptide of SEQ. ID. NO: 7.

212. (Previously presented) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possess at least 96% sequence identity to the polypeptide of SEQ. ID. NO: 7.

213. (Previously presented) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 97% sequence identity to the polypeptide of SEQ. ID. NO: 7.

214. (Previously presented) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 98% sequence identity to the polypeptide of SEQ. ID. NO: 7.

215. (Previously presented) The method of claim 194, wherein said T1R3 is a human T1R3 polypeptide that possesses at least 99% sequence identity to the polypeptide of SEQ. ID. NO: 7.

216. (Canceled)

217. (Currently amended) The method of claim 194 which said T1R3 is encoded by the nucleic acid sequence of SEQ. ID. NO: 9 ~~or SEQ. ID. NO: 11~~.

218. (Currently amended) The method of claim 194 wherein said T1R3 is encoded by a nucleic acid sequence that hybridizes to SEQ. ID. NO: 9 ~~or SEQ. ID. NO: 11~~ under stringent hybridization conditions which are conducting the hybridization reaction at 42°C in a solution comprising 50% formamide, 5X SSC, and 1% SDS and washing at 65°C in a solution comprising 0.2X SSC and 0.1% SDS.

219. (Previously presented) The method of claim 194 wherein said T1R2 and T1R3 sequences are expressed in a cell.

220. (Previously presented) The method of claim 219 wherein said cell is intact or permeabilized.

221. (Previously presented) The method of claim 194 wherein a membrane extract comprises said T1R2/T1R3 receptor.

222. (Previously presented) The method of claim 219 wherein said T1R2 and T1R3 receptor sequences are expressed on the surface of said cell.

223. (Previously presented) The method of claim 219 wherein the cell is a prokaryotic cell.

224. (Previously presented) The method of claim 219 wherein the cell is a eukaryotic cell.

225. (Previously presented) The method of claim 224 wherein the eukaryotic cell is a yeast, insect, amphibian or mammalian cell.

226. (Previously presented) The method of claim 224 wherein the cell is a CHO cell, COS cell, HEK-293 cell or Xenopus oocyte.

227. (Previously presented) The method of claim 219 wherein the cell further expresses a G protein.

228. (Previously presented) The method of claim 227 wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

229. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on the phosphorylation of said T1R2/T1R3 receptor.

230. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on the internalization of said T1R2/T1R3 receptor.

231. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on arrestin translocation.

232. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on second messengers.

233. (Previously presented) The method of claim 232 wherein said second messenger is cAMP, cGMP or IP3.

234. (Previously presented) The method of claim 194 wherein said functional assay detects changes in voltage or intracellular calcium.

235. (Previously presented) The method of claim 234 wherein said functional assay includes the use of a voltage-sensitive or calcium-sensitive dye.

236. (Previously presented) The method of claim 194 wherein the functional assay detects the effect of said compound on G protein activation by said T1R2/T1R3 receptor.

237. (Previously presented) The method of claim 194 wherein said T1R2 and T1R3 sequences are linked to a reporter gene.

238. (Previously presented) The method of claim 237 wherein said reporter gene is luciferase, alkaline, phosphatase or beta-galactosidase.

239. (Previously presented) The method of claim 194 wherein a synthetic compound library comprises said one or more compounds.

240. (Previously presented) The method of claim 194 wherein a combinatorial compound library comprises said one or more compounds.

241. (Previously presented) The method of claim 194 wherein a randomized library of small compounds comprises said one or more compounds.

242. (Previously presented) The method of claim 194 wherein the step of screening is carried out by a high-throughout screening method.

243. (Previously presented) The method of claim 194 wherein the functional assay screens for compounds that enhance or inhibit the activity of the T1R2/T1R3 sweet taste receptor by a sweetener compound.

244. (Previously presented) The method of claim 194 wherein the functional assay screens for compounds that enhance or inhibit the binding of IMP, GMP or an analog thereof to the T1R2/T1R3 sweet taste receptor.

245. (Previously presented) The method of claim 194 wherein the functional assay screens for compounds that enhance the activity of the T1R2/T1R3 sweet taste receptor by saccharin.

246. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on signal transduction.

247. (Previously presented) The method of claim 194 wherein said functional assay detects changes in cellular polarization.

248. (Previously presented) The method of claim 247 wherein said changes are detected by voltage-clamp or patch-clamp technique.

249. (Previously presented) The method of claim 194 wherein the functional assay is a $GTP8_a^{35}S$ assay.

250. (Previously presented) The method of claim 194 wherein said assay is a fluorescent polarization or FRET assay.

251. (Previously presented) The method of claim 194 wherein said assay detects changes in adcenylate cyclase activity.

252. (Previously presented) The method of claim 194 wherein said functional assay detects the effect of said compound on ligand-specific coupling of said T1R2/T1R3 receptor with a G protein.

253. (Currently amended) The method of claim 194 wherein said functional assay detects the effects of said compound on a neurotransmitter or hormone release.

254. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 taste receptor is stably expressed by a cell.

255. (Previously presented) The method of claim 194 wherein said T1R2/T1R3 taste receptor is transiently expressed by a cell.

256. (Previously presented) The method of which 194 wherein said T1R2 and T1R3 sequences are expressed under the control of an inducible promoter.

257-309. (Canceled)

310. (New) The cell of claim 219, wherein the cell is an endogenous taste cell.

311. (New) The cell of claim 310, wherein the cell is a taste cell present in foliate, circumvallate or fungiform papillae.

312. (New) The cell of claim 310, wherein the cell is a taste cell present in geschmackstreifen, oral cavity, gastrointestinal epithelium or epiglottis.

313. (New) The cell of claim 312, wherein the cell is a taste cell present in gastrointestinal epithelium.

314. (New) The cell of claim 221, wherein the cell is an endogenous taste cell.

315. (New) The cell of claim 314, wherein the cell is a taste cell present in foliate, circumvallate or fungiform papillae.

316. (New) The cell of claim 314, wherein the cell is a taste cell present in geschmackstreifen, oral cavity, gastrointestinal epithelium or epiglottis.

317. (New) The cell of claim 316, wherein the cell is a taste cell present in gastrointestinal epithelium.